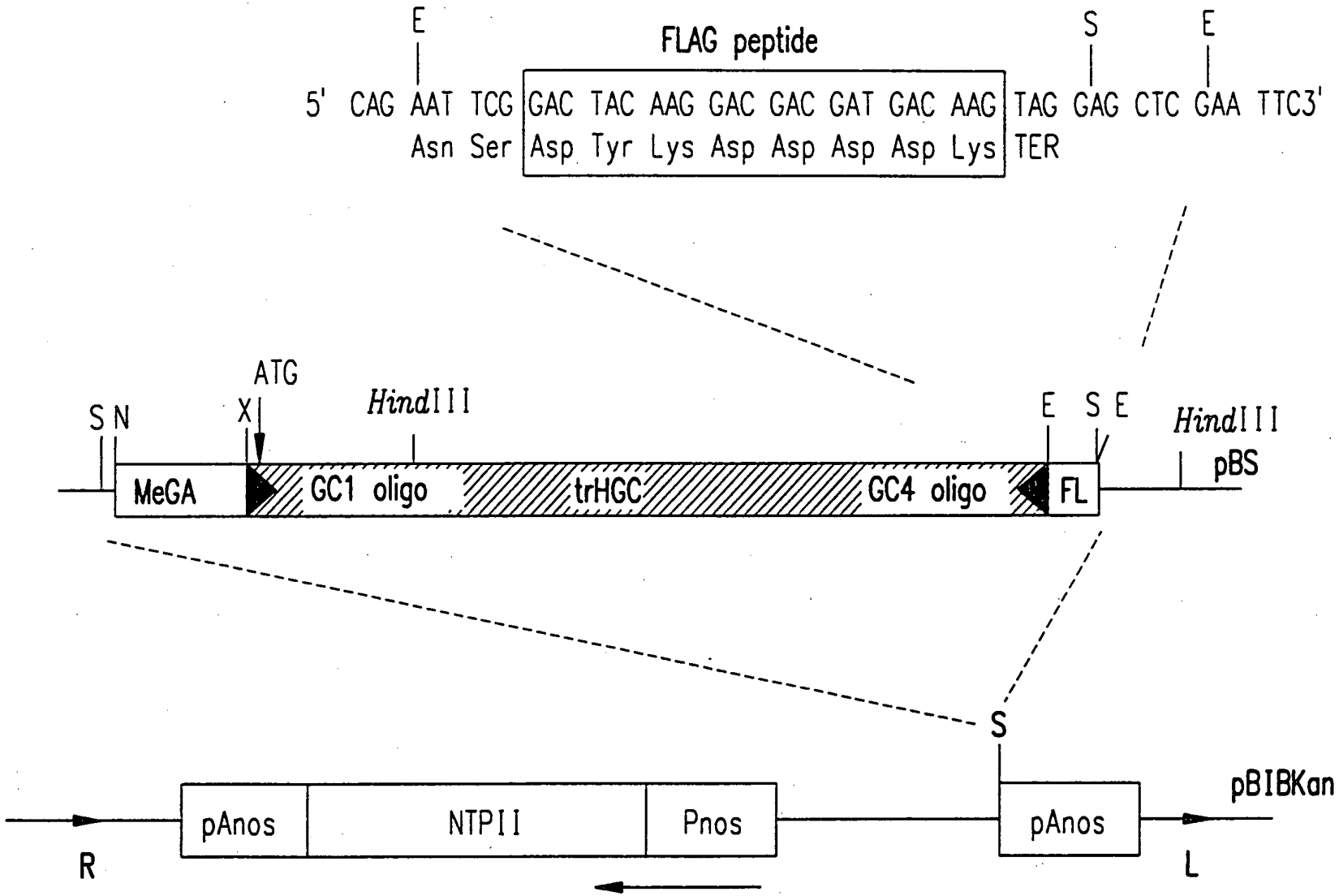

E
FLAG peptide
S
E
5' CAG AAT TCG GAC TAC AAG GAC GAC GAT GAC AAG TAG GAG CTC GAA TTC3'
Asn Ser Asp Tyr Lys Asp Asp Asp Asp Lys TER
ATG
S N
X
HindIII
E S E
HindIII
pBS
MeGA
GC1 oligo
trHGC
GC4 oligo
FL
S
pBIBKan
pAnos
NTPII
Pnos
pAnos
R
L

FIG.1

FIG.2A

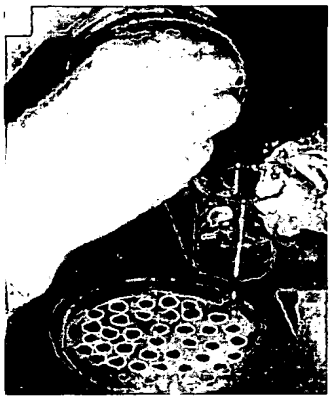


FIG.2B

FIG.2C

FIG.2D

FIG.2E

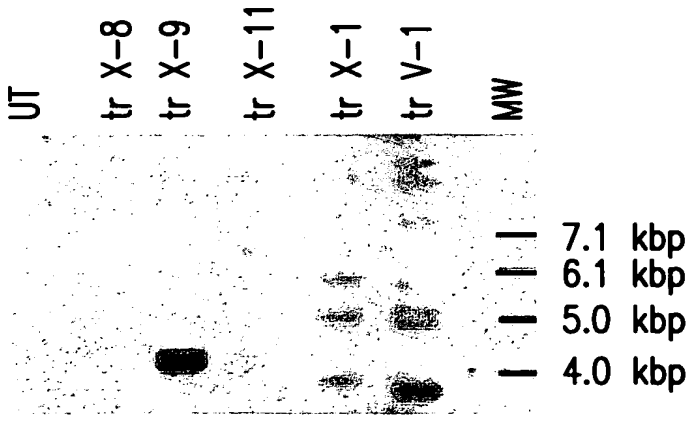


FIG.3

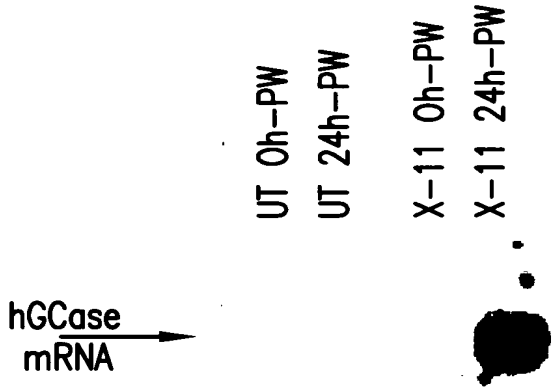


FIG.4

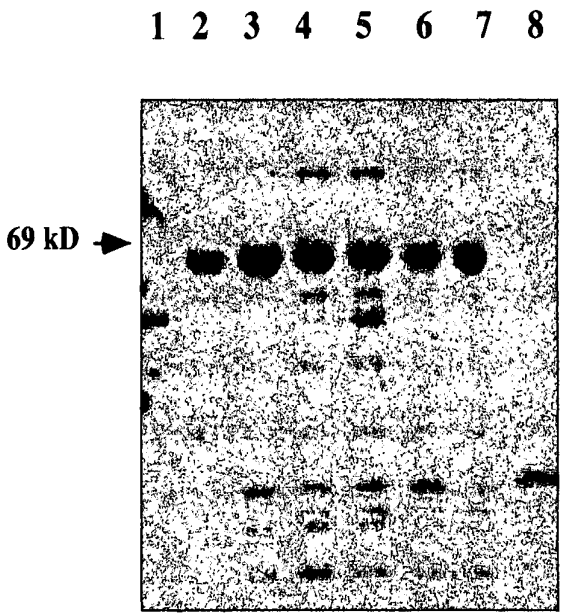


FIG.5A

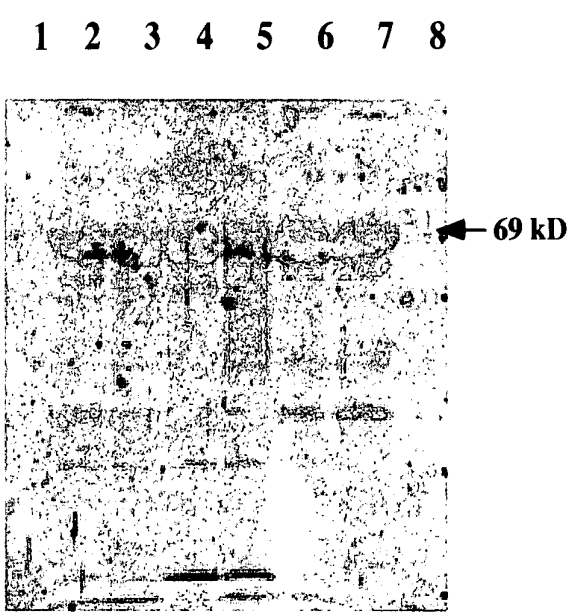


FIG.5B

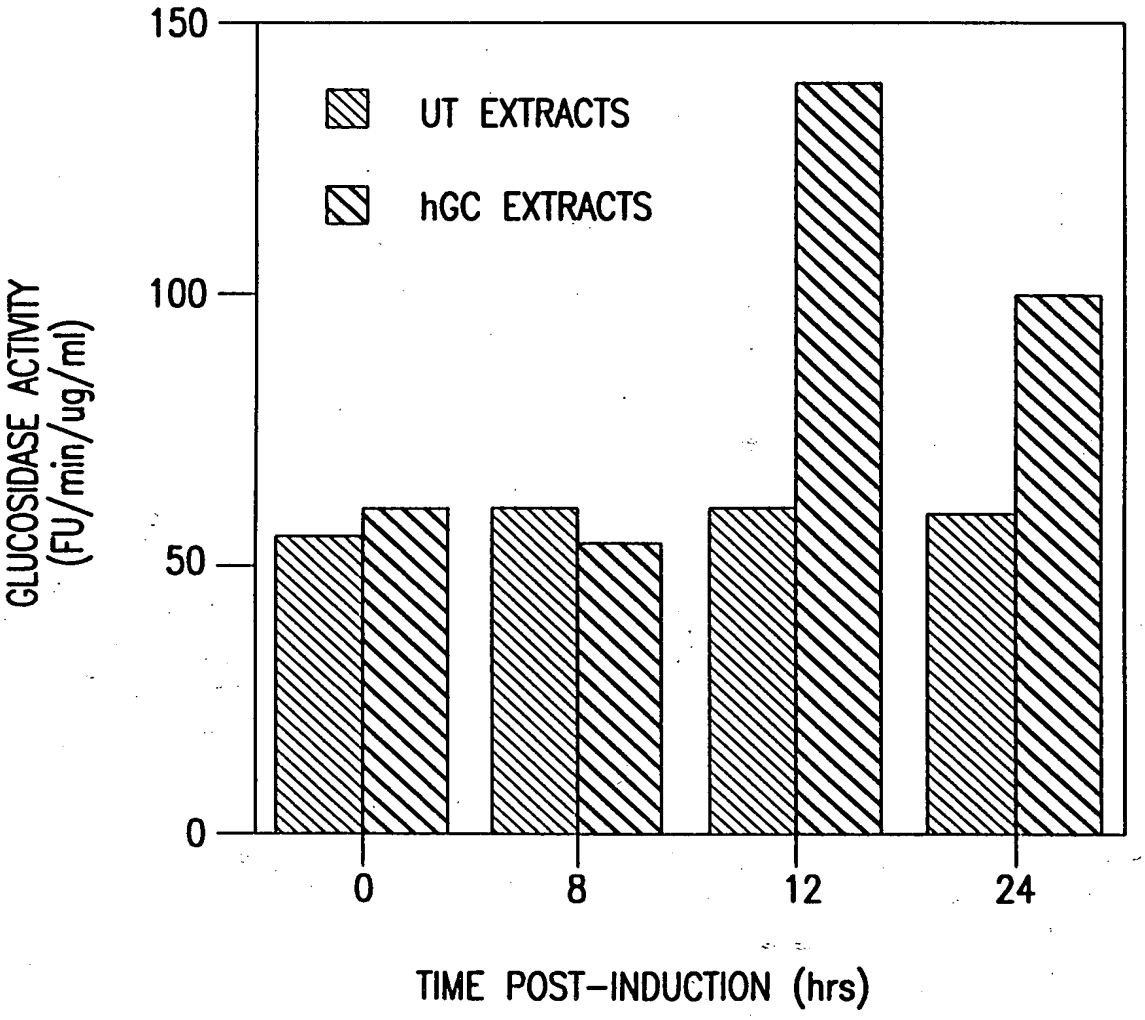

150
100
50
0
UT EXTRACTS
hGC EXTRACTS
GLUCOSIDASE ACTIVITY
(FU/min/ug/ml)
0
8
12
24
TIME POST-INDUCTION (hrs)

FIG.6

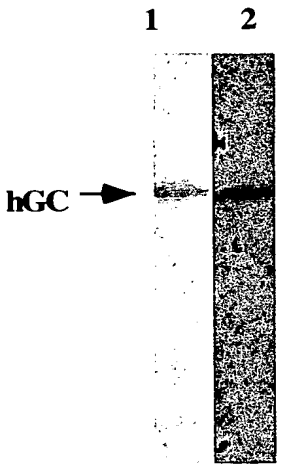


FIG.7A

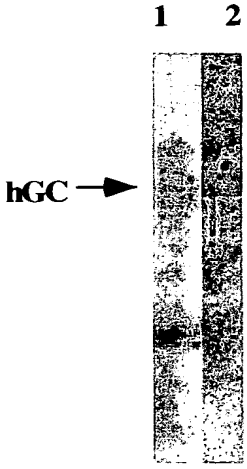


FIG.7B

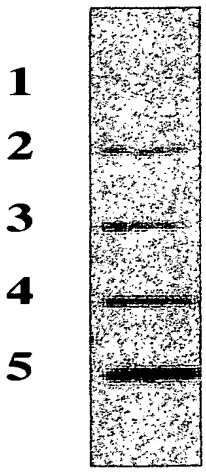


FIG.8A

FIG.8B

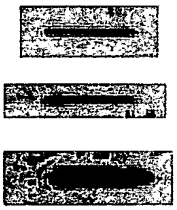


FIG.8C

FIG.9A

```
                                123 ATGGAGTT TTCAAGTCCT TCCAGAGAGG

151  AATGTCCCAA GCCTTTGAGT AGGGTAAGCA TCATGGCTGG CAGCCTCACA

201  GGTTTGCTTC TACTTCAGGC AGTGTCGTGG GCATCAGGTG CCCGCCCCTG

251  CATCCCTAAA AGCTTCGGCT ACAGCTCGGT GGTGTGTGTC TGCAATGCCA

301  CATACTGTGA CTCCTTTGAC CCCCCGACCT TTCCTGCCCT TGGTACCTTC

351  AGCCGCTATG AGAGTACACG CAGTGGGCGA CGGATGGGGC TGAGTATGGG

401  GCCCATCCAG GCTAATCACA CGGGCACAGG CCTGCTACTG ACCCTGCAGC

451  CAGAACAGAA GTTCCAGAAA GTGAAGGGAT TTGGAGGGGC CATGACAGAT

501  GCTGCTGCTC TCAACATCCT TGCCCTGTCA CCCCCTGCCC AAAATTTGCT

551  ACTTAAATCG TACTTCTCTG AAGAAGGAAT CGGATATAAC ATCATCCGGG

601  TACCCATGGC CAGCTGTGAC TTCTCCATCC GCACCTACAC CTATGCAGAC

651  ACCCCTGATG ATTTCCAGTT GCACAACTTC AGCCTCCCAG AGGAAGATAC

701  CAAGCTCAAG ATACCCCTGA TTCACCGAGC CCTGCAGTTG GCCCAGCGTC
```

FIG.9B

```
 751  CCGTTTCACT CCTTGCCAGC CCCTGGACAT CACCCACTTG GCTCAAGACC
 801  AATGGAGCGG TGAATGGGAA GGGGTCACTC AAGGGACAGC CCGGAGACAT
 851  CTACCACCAG ACCTGGGCCA GATACTTTGT GAAGTTCCTG GATGCCTATG
 901  CTGAGCACAA GTTACAGTTC TGGGCAGTGA CAGCTGAAAA TGAGCCTTCT
 951  GCTGGGCTGT TGAGTGGATA CCCCTTCCAG TGCCTGGGCT TCACCCCTGA
1001  ACATCAGCGA GACTTCATTG CCCGTGACCT AGGTCCTACC CTCGCCAACA
1051  GTACTCACCA CAATGTCCGC CTACTCATGC TGGATGACCA ACGCTTGCTG
1101  CTGCCCCACT GGGCAAAGGT GGTACTGACA GACCCAGAAG CAGCTAAATA
1151  TGTTCATGGC ATTGCTGTAC ATTGGTACCT GGACTTTCTG GCTCCAGCCA
1201  AAGCCACCCT AGGGGAGACA CACCGCCTGT TCCCCAACAC CATGCTCTTT
1251  GCCTCAGAGG CCTGTGTGGG CTCCAAGTTC TGGGAGCAGA GTGTGCGGCT
1301  AGGCTCCTGG GATCGAGGGA TGCAGTACAG CCACAGCATC ATCACGAACC
1351  TCCTGTACCA TGTGGTCGGC TGGACCGACT GGAACCTTGC CCTGAACCCC
```

FIG.9C

```
1401  GAAGGAGGAC CCAATTGGGT GCGTAACTTT GTCGACAGTC CCATCATTGT

1451  AGACGTCACC AGGGACACGT TTTACAAACA GCCCATGTTC TACCACCTTG

1501  GCCACTTCAG CAAGTTCATT CCTGAGGGCT CCCAGAGAGT GGGGCTGGTT

1551  GCCAGTCAGA AGAACGACCT GGACGCAGTG GCACTGATGC ATCCCGATGG

1601  CTCTGCTGTT GTGGTCGTGC TAAACCGCTC CTCTAAGGAT GTGCCTCTTA

1651  CCATCAAGGA TCCTGCTGTG GGCTTCCTGG AGACAATCTC ACCTGGCTAC

1701  TCCATTCACA CCTACCTGTG GCGTCGCCAG aattcggact acaaggacga

1751  cgatgacaag tTGA
```

1 50
MEFSSPSREE CPKPLSRVS IMAGSLTGLL LLQAVSWASG ARPCIPKSFG
51 100
YSSVVCVCNA TYCDSFDPP TFPALGTFSR YESTRSGRRM ELSMGPIQAN
101 150
HTGTGLLLTL QPEQKFQKV KGFGGAMTDA AALNILALSP PAQNLLLKSY
151 200
FSEEGIGYNI IRVPMASCD FSIRTYTYAD TPDDFQLHNF SLPEEDTKLK
201 250
IPLIHRALQL AQRPVSLLA SPWTSPTWLK TNGAVNGKGS LKGQPGDIYH
251 300
QTWARYFVKF LDAYAEHKL QFWAVTAENE PSAGLLSGYP FQCLGFTPEH
301 350
QRDFIARDLG PTLANSTHH NVRLLMLDDQ RLLLPHWAKV VLTDPEAAKY
351 400
VHGIAVHWYL DFLAPAKAT LGETHRLFPN TMLFASEACV GSKFWEQSVR
401 450
LGSWDRGMQY SHSIITNLL YHVVGWTDWN LALNPEGGPN WVRNFVDSPI
451 500
IVDVTKDTFY KQPMFYHLG HFSKFIPEGS QRVGLVASQK NDLDAVALMH
501 550
PDGSAVVVVL NRSSKDVPL TIKDPAVGFL ETISPGYSIH TYLWRRQnsd

ykddddk"

FIG.10

60

CAATACGATA TTACCGAATA TTATACTAAA TCAAAATTTA ATTTATCATA TCGAATTATT

120

AAACTGATAT TTCAAATTTT AATATTTAAT ATCTACTTTC AACTATTATT ACCTAATTAT

180

CAAATGCAAA ATGTATGAGT TATTTCATAA TAGCCCGAGT TCGTATCCAA ATATTTTACA

240

CTTGACCAGT CAACTTGACT ATATAAAACT TTACTTCAAA AAATTAAAAA AAAAAGAAAG

300

TATATTATTG TAAAAGATAA TACTCCATTC AAAATATAAA ATGAAAAAAG TCCAGCGCGG

360

CAACCGGGTT CCTCTATAAA TACATTTCCT ACATCTTCTC TTCTCCTCAC ATCCCATCAC

420

TCTTCTTTTA ACAATTATAC TTGTCAATCA TCAATCCCAC AAACAACACT TTTTCTCTCC

471

TCTTTTTCCT CACCGGCGGC AGACTTACCG GTGAAATCTA GAGTAAGCAT C

FIG. 11

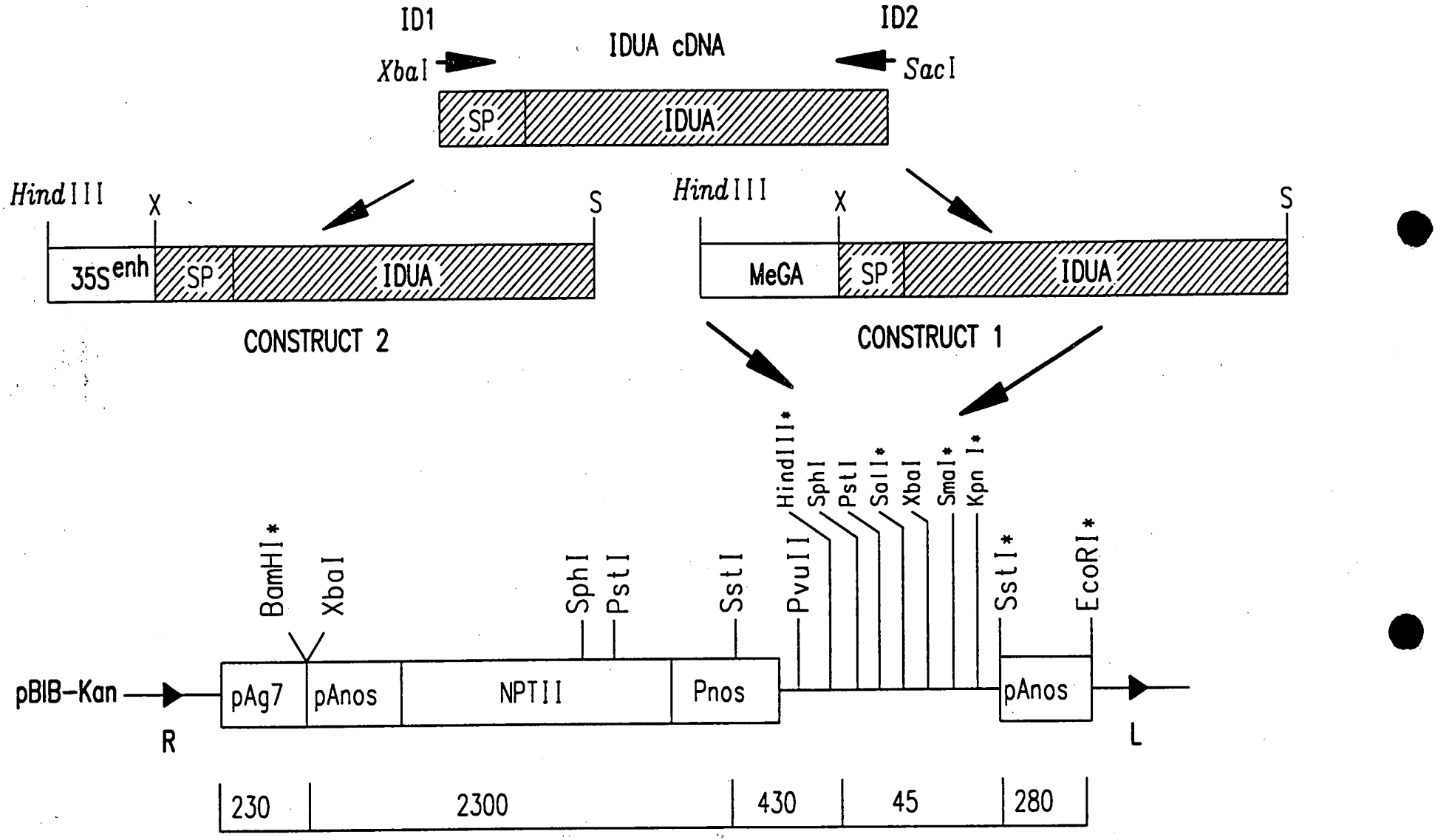
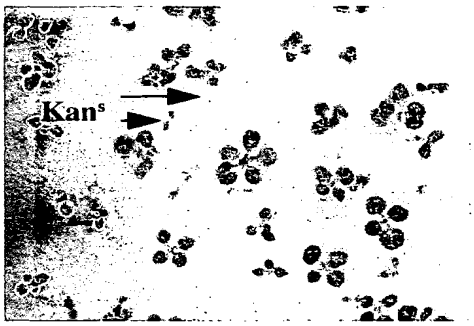

ID1
IDUA cDNA
ID2
XbaI
SacI
SP
IDUA
HindIII
X
S
35S enh
SP
IDUA
CONSTRUCT 2
HindIII
X
S
MeGA
SP
IDUA
CONSTRUCT 1
HindIII*
SphI
PstI
SalI*
XbaI
SmaI*
Kpn I*
BamHI*
XbaI
SphI
PstI
SstI
PvuII
SstI*
EcoRI*
pBIB-Kan
R
pAg7
pAnos
NPTII
Pnos
pAnos
L
230
2300
430
45
280

FIG.12

FIG.13A



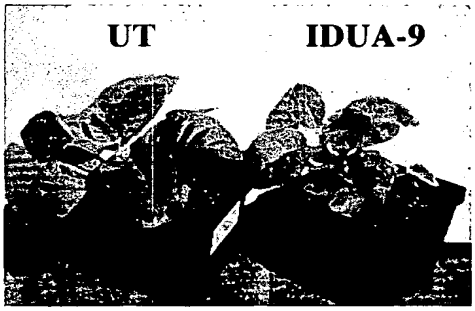


FIG.13B

FIG.13C

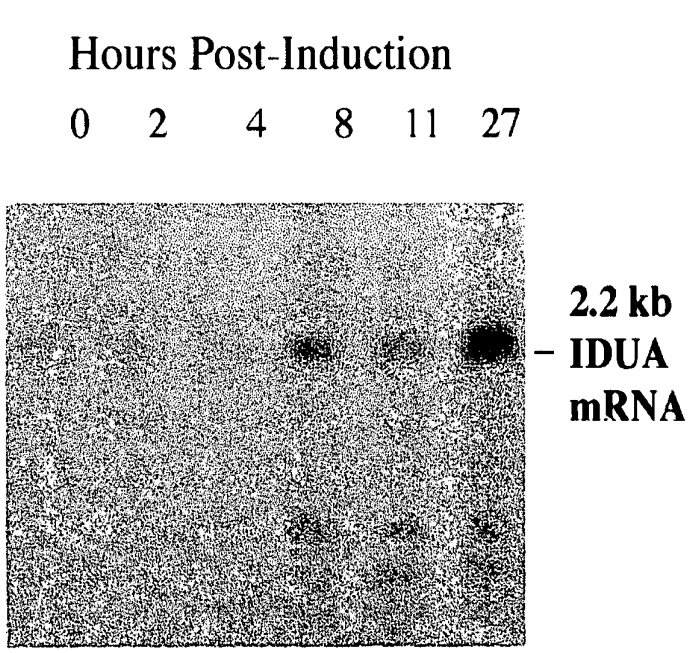


FIG.14A

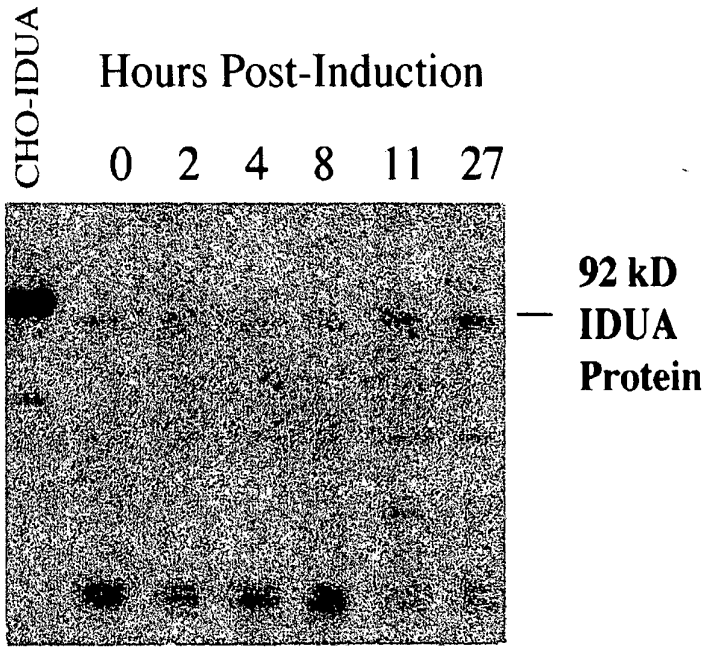


FIG.14B

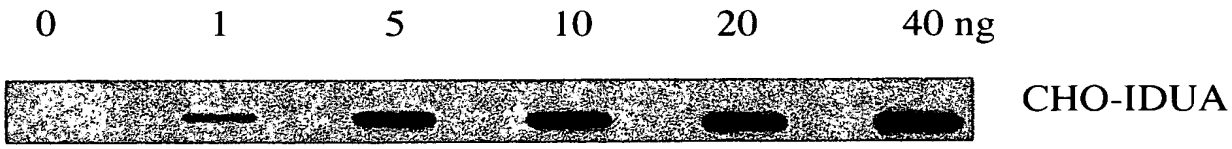


FIG.15A

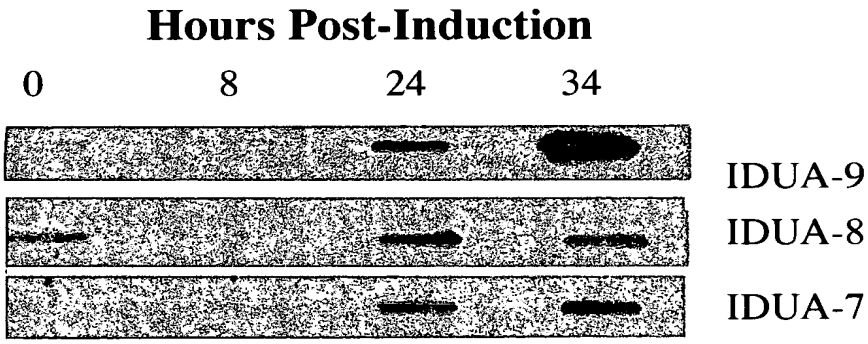


FIG.15B

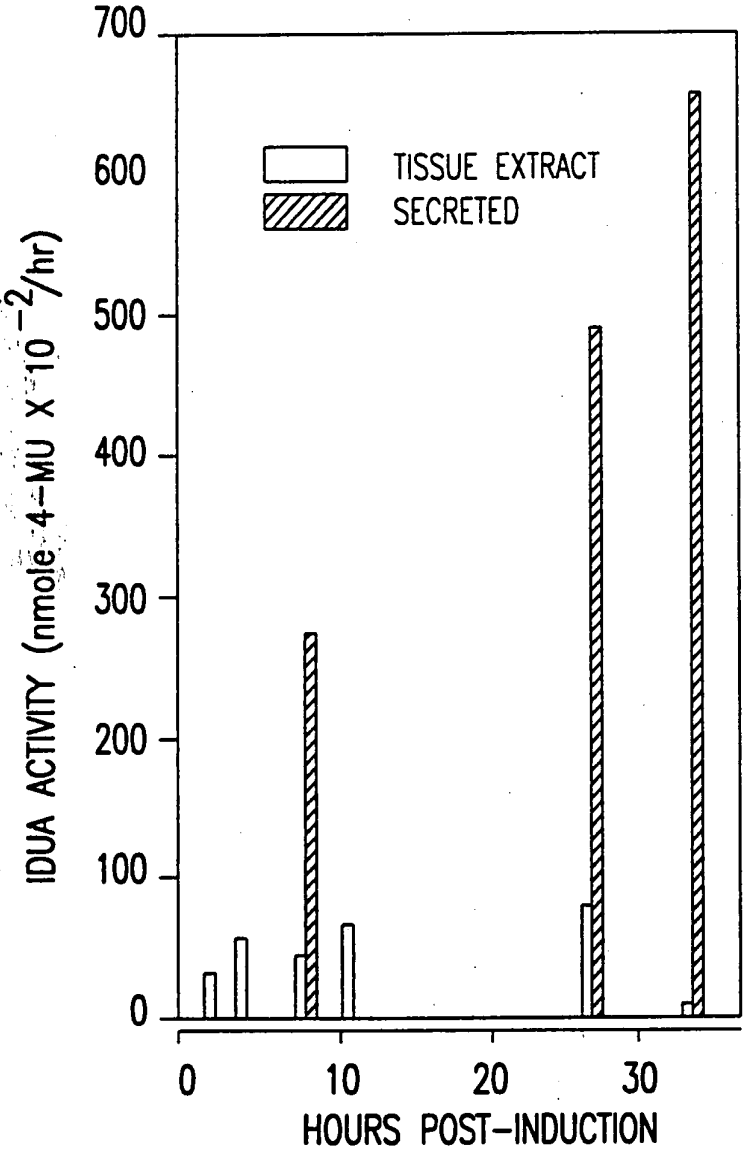


FIG.16A

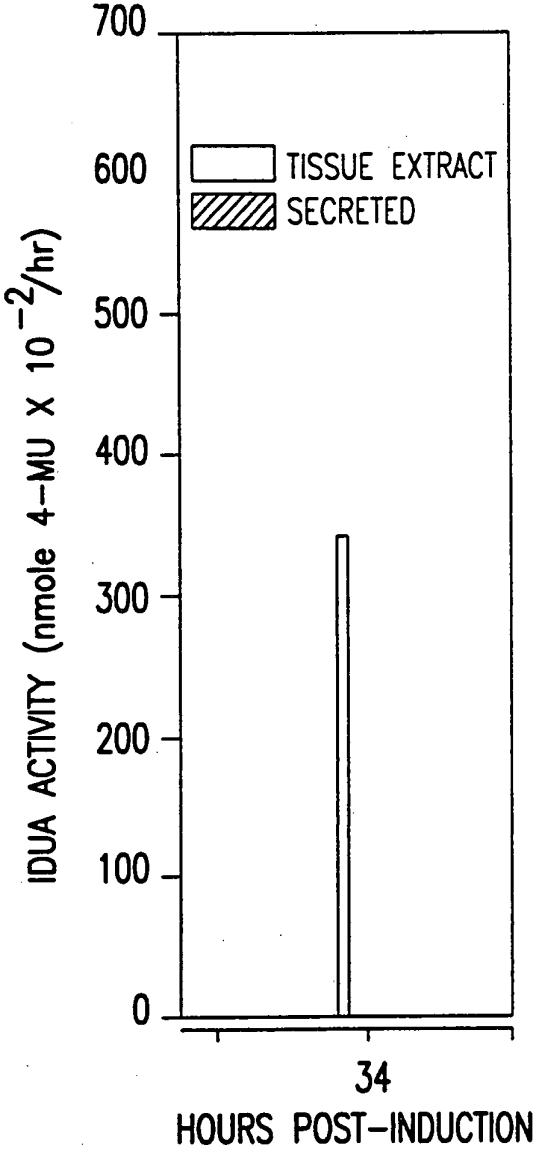


FIG.16B

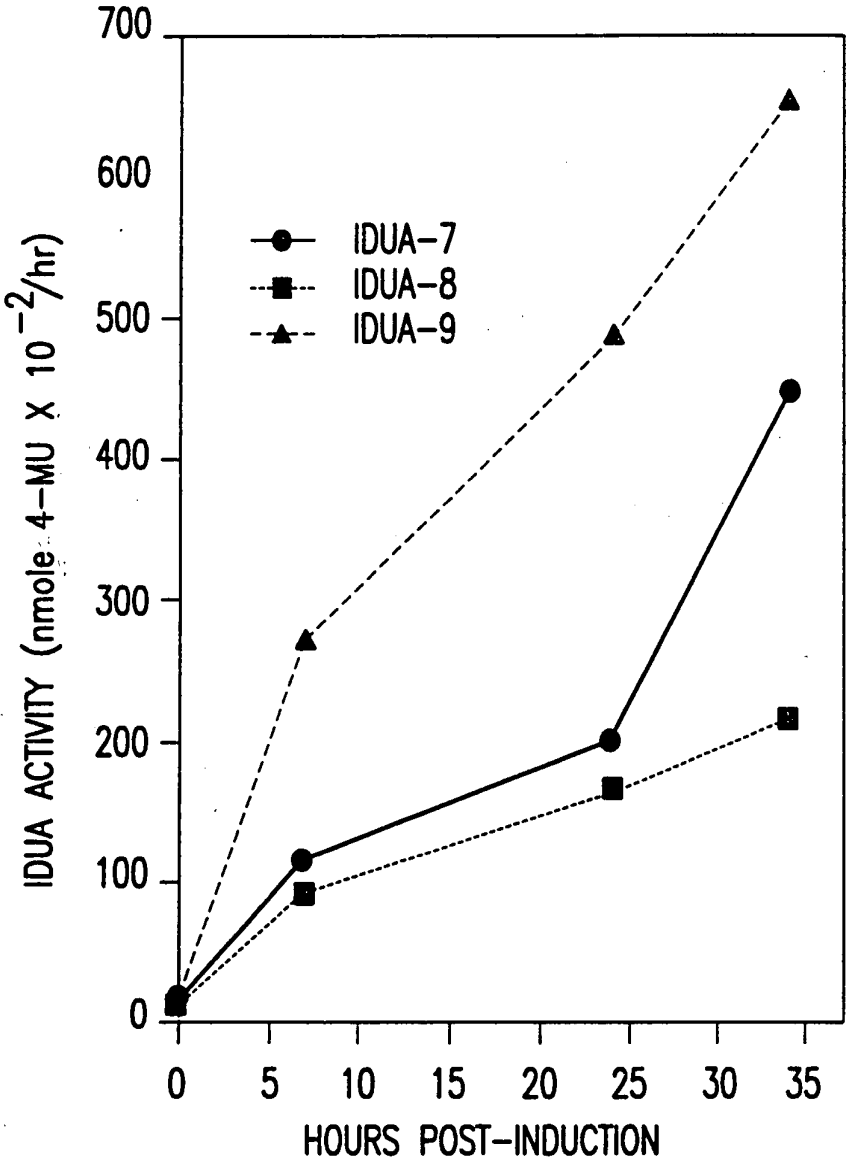


FIG.17A

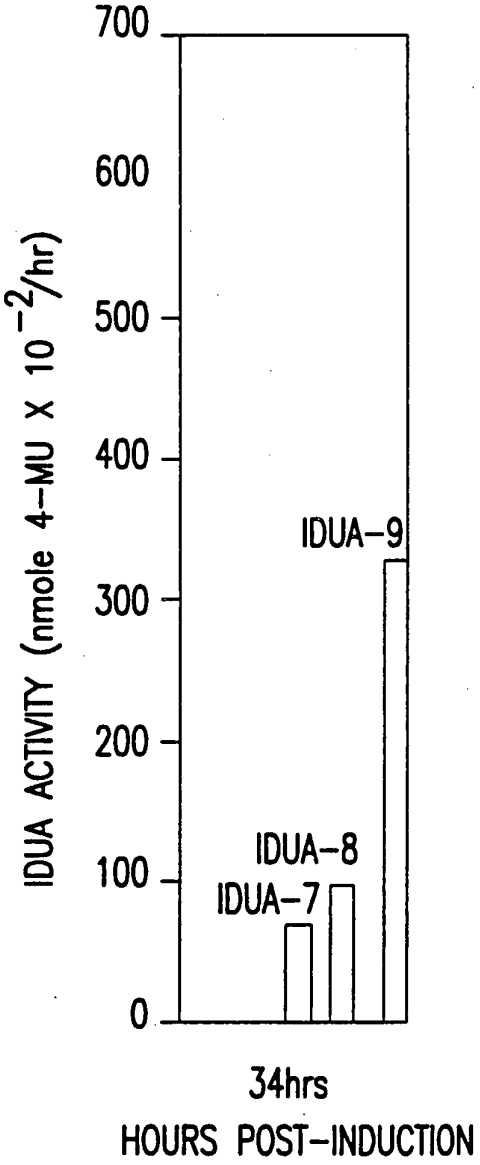


FIG.17B

1 2 3

24 26 36

Hours Post-Induction

FIG. 18

```
                                   90                  110
                                   ATGCGTCCCCTGCGCCCCCGCGCCGCGCTGCT

          130                      150                 170
GGCGCTCCTGGCCTCGCTCCTGGCCGCGCCCCCGGTGGCCCCGGCCGAGGCCCCGCACCT

          190                      210                 230
GGTGCAGgTGGACGCGGCCCGCGCGCTGTGGCCCCTGCGGCGCTTCTGGAGGAGCACAGG

          250                      270                 290
CTTCTGCCCCCCGCTGCCACACAGCCAGGCTGACCAGTACGTCCTCAGCTGGGACCAGCA

          310                      330                 350
GCTCAACCTCGCCTATGTGGGCGCCGTCCCTCACCGCGGCATCAAGCAGGTCCGGACCCA

          370                      390                 410
CTGGCTGCTGGAGCTTGTCACCACCAGGGGGTCCACTGGACGGGGCCTGAGCTACAACTT

          430                      450                 470
CACCCACCTGGACGGGTACTTGGACCTTCTCAGGGAGAACCAGCTCCTCCCAGGGTTTGA
```

FIG.19A

490 510 530
GCTGATGGGCAGCGCCTCGGGCCACTTCACTGACTTTGAGGACAAGCAGCAGGTGTTTGA

550 570 590
GTGGAAGGACTTGGTCTCCAGCCTGGCCAGGAGATACATCGGTAGGTACGGACTGGCGCA

610 630 650
TGTTTCCAAGTGGAACTTCGAGACGTGGAATGAGCCAGACCACCACGACTTTGACAACGT

FIG.19B

670 690 710
CTCCATGACCATGCAAGGCTTCCTGAACTACTACGATGCCTGCTCGGAGGGTCTGCGCGC

730 750 770
CGCCAGCCCCGCCCTGCGGCTGGGAGGCCCCGGCGACTCCTTCCACACCCCACCGCGATC

790 810 830
CCCGCTGAGCTGGGGCCTCCTGCGCCACTGCCACGACGGTACCAACTTCTTCACTGGGGA

850 870 890
GGCGGGCGTGCGGCTGGACTACATCTCCCTCCACAGGAAGGGTGCGCGCAGCTCCATCTC

910 930 950
CATCCTGGAGCAGGAGAAGGTCGTCGCGCA**cg**AGATCCGGCAGCTCTTCCCCAAGTTCGC

970 990 1010
GGACACCCCCATTTACAACGACGAGGCGGACCCGCTGGTGGGCTGGTCCCTGCCACAGCC

FIG.19C

1030 1050 1070
GTGGAGGGCGGACGTGACCTACGCGGCCATGGTGGTGAAGGTCATCGCGCAGCATCAGAA

1090 1110 1130
CCTGCTACTGGCCAACACCACCTCCGCCTTCCCCTACGCGCTCCTGAGCAACGACAATGC

1150 1170 1190
CTTCCTGAGCTACCACCCGCACCCCTTCGCGCAGCGCACGCTCACCGCGCGCTTCCAGGT

1210 1230 1250
CAACAACACCCGCCCGCCGCACGTGCAGCTGTTGCGCAAGCCGGTGCTCACGGCCATGGG

1270 1290 1310
GCTGCTGGCGCTGCTGGATGAGGAGCAGCTCTGGGCCGAAGTGTCGCAGGCCGGGACCGT

1330 1350 1370
CCTGGACAGCAACCACACGGTGGGCGTCCTGGCCAGCGCCCACCGCCCCCAGGGCCCGGC

1390 1410 1430
CGACGCCTGGCGCGCCGCGGTGCTGATCTACGCGAGCGACGACACCCGCGCCCACCCCAA

FIG.19D

1450 1470 1490
CCGCAGCGTCGCGGTGACCCTGCGGCTGCGCGGGGTGCCCCCCGGCCCGGGCCTGGTCTA

1510 1530 1550
CGTCACGCGCTACCTGGACAACGGGCTCTGCAGCCCCGACGGCGAGTGGCGGCGCCTGGG

1570 1590 1610
CCGGCCCGTCTTCCCCACGGCAGAGCAGTTCCGGCGCATGCGCGCGGCTGAGGACCCGGT

34

1630 1650 1670
GGCCGCGGCGCCCCGCCCCTTACCCGCCGGCGGCCGCCTGACCCTGCGCCCCGCGCTGCG

1690 1710 1730
GCTGCCGTCGCTTTTGCTGGTGCACGTGTGTGCGCGCCCCGAGAAGCCGCCCGGGCAGGT

1750 1770 1790
CACGCGGCTCCGCGCCCTGCCCCTGACCCAAGGGCAGCTGGTTCTGGTCTGGTCGGATGA

FIG.19E

1810 1830 1850
ACACGTGGGCTCCAAGTGCCTGTGGACATACGAGATCCAGTTCTCTCAGGACGGTAAGGC

1870 1890 1910
GTACACCCCGGTCAGCAGGAAGCCATCGACCTTCAACCTCTTTGTGTTCAGCCCAGACAC

1930 1950 1970
AGGTGCTGTCTCTGGCTCCTACCGAGTTCGAGCCCTGGACTACTGGGCCCGACCAGGCCC

1990 2010 2030
CTTCTCGGACCCTGTGCCGTACCTGGAGGTCCCTGTGCCAAGAGGGCCCCCATCCCCGGG

2050 2070 2090

CAATCCATGAGCCTGTGCTGAGCCCCAGTGGGTTGCACCTCCACCGGCAGTCAGCGAGCT

2110 2130 2150

GGGGCTGCACTGTGCCCATGCTGCCCTCCCATCACCCCCTTTGCAATATATTTTT

FIG.19F

```
        10                  30                  50
MRPLRPRAALLALLASLLAAPPVAPAEAPHLVHVDAARALWPLRRFWRSTGFCPPLPHSQ

        70                  90                  110
ADQYVLSWDQQLNLAYVGAVPHRGIKQVRTHWLLELVTTRGSTGRGLSYNFTHLDGTLDL

        130                 150                 170
LRENQLLPGFELMGSASGHFTDFEDKQQVFEWKDLVSSLARRYIGRYGLAHVSKWNFETW

        190                 210                 230
NEPDHHDFDNVSMTMQGFLNYYDACSEGLRAASPALRLGGPGDSFHTPPRSPLSWGLLRH

        250                 270                 290
CHDGTNFFTGEAGVRLDYISLHRKGARSSISILEQEKVVAQEIRQLFPKFADTPIYNDEA

        310                 330                 350
DPLVGWSLPQPWRADVTYAAMVVKVIAQHQNLLLANTTSAFPYALLSNDNAFLSYHPHPF

        370                 390                 410
AQRTLTARFQVNNTRPPHVQLLRKPVLTAMGLLALLDEEQLWAEVSQAGTVLDSNHTVGV
```

FIG.20A

```
        430                   450                   470
LASAHRPQGPADAWRAAVLIYASDDTRAHPNRSVAVTLRLRGVPPGPGLVYVTRYLDNGL

        490                   510                   530
CSPDGEWRRLGRPVFPTAEQFRRMRAAEDPVAAAPRPLPAGGRLTLRPALRLPSLLLVHV

        550                   570                   590
CARPEKPPGQVTRLRALPLTQGQLVLVWSDEHVGSKCLWTYEIQFSQDGKAYTPVSRKPS

        610                   630                   650
TFNLFVFSPDTGAVSGSYRVRALDYWARPGPFSDPVPYLEVPVPRGPPSPGNP
```

FIG.20B

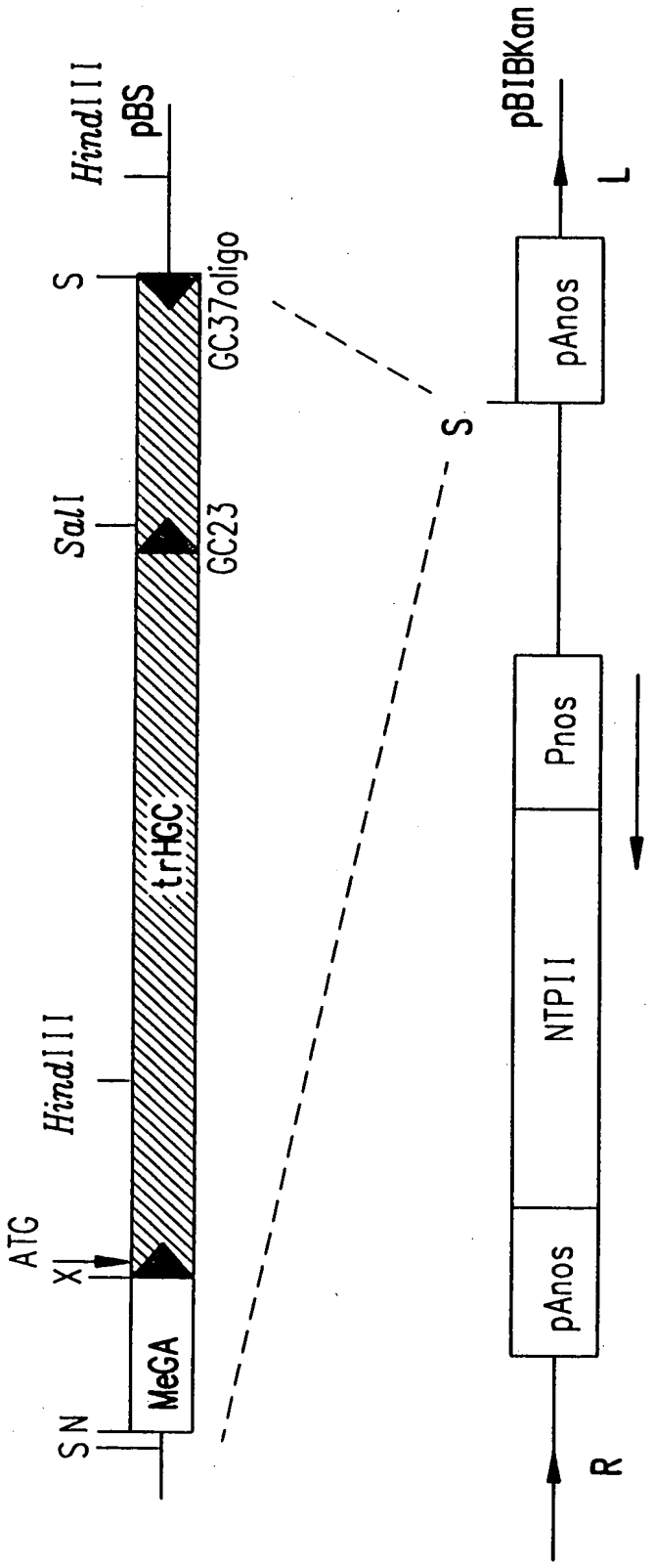

pBIBKan
L
pAnos
S
Pnos
NTPII
pAnos
R
S
GC37oligo
pBS
HindIII
S
SalI
GC23
trHGC
HindIII
ATG
X
MeGA
SN

FIG.21